

COVID-19 Information

[Public health information \(CDC\)](#)

[Research information \(NIH\)](#)

[SARS-CoV-2 data \(NCBI\)](#)

[Prevention and treatment information \(HHS\)](#)

[Español](#)

BLAST® » [blastp suite-2sequences](#) » results for RID-TAJDJG4E114

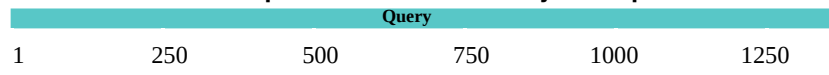
Job Title [SepA Shigella Flexneri - EC092 ...](#)
 RID [TAJDJG4E114](#) Search expires on 11-19 01:28 am
 Program Blast 2 sequences
 Query ID [CAA88252.1](#) (amino acid)
 Query Descr [sepA \[Shigella flexneri 5a str. M90T\] ...](#)
 Query Length 1366
 Subject ID lcl|Query_14487 (amino acid)
 Subject Descr [None ...](#)
 Subject Length 1364

Descriptions

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
unnamed protein product		2717	2717	100%	0.0	98.39%	1364	Query_14487

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



Alignments

Alignment view CDS feature

unnamed protein product

Sequence ID: Query_14487 Length: 1364 Number of Matches: 1
 Range 1: 1 to 1364

Score	Expect	Method	Identities	Positives	Gaps	Frame
2717 bits(7044)	0.0()	Compositional matrix adjust.	1344/1366(98%)	1347/1366(98%)	2/1366(0%)	
Query	1	MNKIYYLK YCHITKSLIAVSELARRVTCKSHRRLSRRVILTSVAALSLSSAWPALSATVS	60			60
Sbjct	1				60
Query	61	AEIPYQIFRDF AENKGQFTP GTTNI SIYDKQGNLVGKLDKAPMADFSSATIT TGS LPPGD	120			120
Sbjct	61N				120
Query	121	HTLYSPQYVVTAKHVSGSDTMSFGYAKNTYAVGTNNNSGLDIKTRRLSKLVTEVAPAEV	180			180
Sbjct	121				180
Query	181	SDIGAVSGAYQAGGRFTEFYRLGGMQYVKDKNGNRTQVYTNGGFLVGGTVSALNSYNNG	240			240
Sbjct	181A.....				240
Query	241	QMITAQTGDI FLIPNGPLANYLNMGDSGSPLFAYDSLQKKWVLIGVLS SGTNYGNNWV	300			300
Sbjct	241-N.A.....				299
Query	301	TTQDFLGGQQPQND FDKTIA YTS GEGVLQWKYDAANGTGLTQGNTTWGYAWKERKLILNA	360			360

Sbjct	300DMHG.KGN-D	358
Query	361	GKNLLFTGNNGEVVLQNSVNGAGYLQFAGDYRVSALNGQTMGGGIITDKGTHVLWQVN	420
Sbjct	359	418
Querv	421	GVAGDNLHKTGEGTLTVNGTGVNAGGLKVGDTVILNQADRDKVQAFSSVGIASGRPT	480
Sbjct	419A	478
Querv	481	VVLSDSQVNPDNISWGYRGGRELENGNLTFFTRLQAADYGAIITNNSEKKSTVTLDLQT	540
Sbjct	479N	538
Query	541	LKASDINVPVNTVSIFGGRGAPGDLYYDSSTKQYFILKASSYSPFFSDLNSSVWQNVGK	600
Sbjct	539	598
Querv	601	DHNKAIDTVKQKIEASSQPYMYHGQLNGNMDVNIPQLSGKDV LALDGSVNLPEGSITKK	660
Sbjct	599	.R	658
Query	661	SGTLIFQGHPIHAGTTSSSQSDWETRQFTLEKLLDAATFHLSRNGKMQGDINATNGS	720
Sbjct	659	718
Query	721	TVILGSSRVFTDRSDGTNAVSSVEGSATATTVGQSDYSGNVTLENKSSLQIMERFTGG	780
Sbjct	719	778
Query	781	IEAYDSTVSVTSQNAVFDVRVGSFVNSSLTLGKGAKLTAQSGIFSTGAVDVKENASLTLTG	840
Sbjct	779	838
Querv	841	MPSAQKQGYSPVISTTEGINLEDNASFSVKNMGYLSDDIHAGTTAATINLGSDADAGK	900
Sbjct	839K	898
Querv	901	TDSPLFSSLMKGYNAVLRGSITGAQSTVNMINALWYSDGKSEAGALKAKGSRIELGDGKH	960
Sbjct	899T	958
Querv	961	FATLQVKELADNTTFLMHTNNSRADQLNVTDKLSGSNNSVLVDFLNKPASEMSVTLITA	1020
Sbjct	959W	1018
Query	1021	PKGSDEKFTTAGTQQIGFSNVTPVISTEKTDATKWVLTGYQTTADAGASKAAKDFMASG	1080
Sbjct	1019	1078
Query	1081	YKSFLTEVNNLNKRMGDLRDTQGDAGVWARIMNGTGSADGDYSDNYTHVQIGVDRKHELD	1140
Sbjct	1079	1138
Query	1141	GVDLFTGALLTYTDSNASSHAFSGKNKSVGGGLYASALFNSGAYFDLIGKYLHHDNQHTA	1200
Sbjct	1139T	1198
Querv	1201	NFASLGTKDYSSHSWYAGAEVGYRYHLTKESWVEPQIELVYGSVSGKAFSWEARGMALSM	1260
Sbjct	1199D	1258
Query	1261	KDKDYNPLIGRTGVDVGRVAFSGDDWKITARAGLGYQFDLLANGETVLQDASGEKRFEGEK	1320
Sbjct	1259	1318
Query	1321	DSRMLMTVGMNAEIKDNMRLGLELEKSAFGKYNVDNAINANFRYVF	1366
Sbjct	1319	1364

Taxonomy

Reports

- **Lineage**
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Dot Plot

Plot of CAA88252.1 vs Icl|Query_14487

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